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ENTERED

## RAW SEQUENCE LISTING

DATE: 03/11/2002

PATENT APPLICATION: US/09/846,589A

TIME: 09:44:16

Input Set : A:\BB-1191 Seq List.txt

Output Set: N:\CRF3\03112002\I846589A.raw

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3 <110> APPLICANT: Famodu, Layo O.
4      Orozco, Buddy
5      Rafalski, Antoni
7 <120> TITLE OF INVENTION: Plant Aminoacyl-tRNA Synthetase
9 <130> FILE REFERENCE: BB-1191
C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/846,589A
C--> 12 <141> CURRENT FILING DATE: 2002-01-22
14 <150> PRIOR APPLICATION NUMBER: 60/092,866
W--> 15 <151> PRIOR FILING DATE: July 15, 1998
17 <160> NUMBER OF SEQ ID NOS: 29
19 <170> SOFTWARE: Microsoft Office 97
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 1948
23 <212> TYPE: DNA
24 <213> ORGANISM: Zea mays
26 <400> SEQUENCE: 1
27 cgacgatag ccgcccgcgt cgaccagagc actcccccg cgtcgccacg atgtcgtctg 60
28 agcctccacc cgctcctct gccgcccgc gagaggaact cgctgctgac ctttccgccg 120
29 ctaccctcag caagaagcag cagaagaagg acgcgaggaa ggcggagaag gcagagcagc 180
30 gccagcgta gcagcagcag cagcagcagc cggcgagcgc cgaggacccg ttcgcggcca 240
31 actacggcga ggtccccgctc gaggagatcc agtcaaaggc catctccggc cgctcgtggt 300
32 cccatgtcgg cgacctcgac gactccgctc cgggcccgtc cgtgcttatt cgcggagccg 360
33 cgcaggccat ccgtccggtc agcaagaaga tggcttctc cgtgctgcgc cagagtatga 420
34 gcaccgtgca gtgcgtgctc gtcgccagcg ccgacgccg cgtcagcacg cagatggtgc 480
35 gcttcgccac cgccctcagc aaggagtcca tcgtcgacgt tgaggcgctc gtctccctcc 540
36 caaaggagcc cctcaaggcc accacacagc aggttgagat ccaagtgagg aagatctatt 600
37 gcatcaatag ggctattccg acccttccaa ttaacctga agatgcgctc cggagtgagg 660
38 cagattttga gaaggctgaa ttggctggag aaaagcttgt tcgcgttggc caagataccc 720
39 gcttgaacta cagagctatt gatctacgaa caccctcgaa tcaagccata ttccggatcc 780
40 agtgtcaagt tgaaaacaaa tttagagatt ttttgttgct gaagaacttt gtcgggatcc 840
41 acaccccaaa attgatttct ggatctagtg aagggggtgc ggctgtattc aagcttctgt 900
42 acaatggtca acctgcttgt ttggcacaat cccctcagtt atacaagcaa atggctatct 960
43 ctggtggttt tgagcgagta tttgaggtcg gccctgtggt tagagcagaa aattcaaaaca 1020
44 cacacaggca tctatgtgag ttcgttggtc ttgatgctga aatggagatt aaggagcatt 1080
45 attttgaggt ctgtgacatt atagatggct tattcgtatc aatattttaa cacttgctctg 1140
46 aaaactgcaa gaaagaactc gaatcaataa acaggcagta tccatttgaa cctctgaagt 1200
47 atctagacaa aacctttaag ctcaattatg aagaaggaat tcaaatgttg aaggaagccg 1260
48 gaacagaaat cgagcctatg ggtgacctca ataccgaagc tgagaaaaaa cttggtcggc 1320
49 ttgtcaggga aaagtatgac acagattttt tcatcctgta tcggtatcct ttggctgtac 1380
50 gtcggttcta caccatgcct tgttatgaca acccagcgta caccaattct tttgatgtct 1440
51 tcattcgagg cgaggagata atatctggag cacaaaggat acacactcct gagctgctgg 1500
52 ccaagcgcg cagcagagtgt ggaatcgacg tgagcactat ctcggcctac attgaatcct 1560
53 tcagctatgg cgtgccgcca cacggcggtt tcgggggtggg tttggagagg gtggtgatgc 1620

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54 tgttctgtgc cctgaacaac atcaggaaga cctccctgtt cccgcgcgac ccgcagaggc 1680
55 tcgtgccgta agtttctgat tccaagcctg agtcttcgag tggctctacgg agcagatccg 1740
56 atgttggttac catcagagtt gacttgcaat cttagctcct gaacctggcg gttaccgtgg 1800
57 atcagagttc ctgttgaatt tcacaaaagc ctacttggtc ctaatagatt gctgcaacca 1860
58 acaatattac gaccctttcg ggctttttctt cccgcctcac gtgttattct ggtctatact 1920
59 tgtttttaag tgcaagtatt gctcagtt 1948
61 <210> SEQ ID NO: 2
62 <211> LENGTH: 546
63 <212> TYPE: PRT
64 <213> ORGANISM: Zea mays
66 <400> SEQUENCE: 2
67 Met Ser Ser Glu Pro Pro Pro Ala Ser Ser Ala Ala Ala Gly Glu Glu
68 1 5 10 15
70 Leu Ala Ala Asp Leu Ser Ala Ala Thr Leu Ser Lys Lys Gln Gln Lys
71 20 25 30
73 Lys Asp Ala Arg Lys Ala Glu Lys Ala Glu Gln Arg Gln Arg Gln Gln
74 35 40 45
76 Gln Gln Gln Gln Gln Pro Ala Asp Ala Glu Asp Pro Phe Ala Ala Asn
77 50 55 60
79 Tyr Gly Glu Val Pro Val Glu Glu Ile Gln Ser Lys Ala Ile Ser Gly
80 65 70 75 80
82 Arg Ser Trp Ser His Val Gly Asp Leu Asp Asp Ser Ala Ala Gly Arg
83 85 90 95
85 Ser Val Leu Ile Arg Gly Ala Ala Gln Ala Ile Arg Pro Val Ser Lys
86 100 105 110
88 Lys Met Ala Phe Val Val Leu Arg Gln Ser Met Ser Thr Val Gln Cys
89 115 120 125
91 Val Leu Val Ala Ser Ala Asp Ala Gly Val Ser Thr Gln Met Val Arg
92 130 135 140
94 Phe Ala Thr Ala Leu Ser Lys Glu Ser Ile Val Asp Val Glu Gly Val
95 145 150 155 160
97 Val Ser Leu Pro Lys Glu Pro Leu Lys Ala Thr Thr Gln Gln Val Glu
98 165 170 175
100 Ile Gln Val Arg Lys Ile Tyr Cys Ile Asn Arg Ala Ile Pro Thr Leu
101 180 185 190
103 Pro Ile Asn Leu Glu Asp Ala Ala Arg Ser Glu Ala Asp Phe Glu Lys
104 195 200 205
106 Ala Glu Leu Ala Gly Glu Lys Leu Val Arg Val Gly Gln Asp Thr Arg
107 210 215 220
109 Leu Asn Tyr Arg Ala Ile Asp Leu Arg Thr Pro Ser Asn Gln Ala Ile
110 225 230 235 240
112 Phe Arg Ile Gln Cys Gln Val Glu Asn Lys Phe Arg Asp Phe Leu Leu
113 245 250 255
115 Ser Lys Asn Phe Val Gly Ile His Thr Pro Lys Leu Ile Ser Gly Ser
116 260 265 270
118 Ser Glu Gly Gly Ala Ala Val Phe Lys Leu Leu Tyr Asn Gly Gln Pro
119 275 280 285
121 Ala Cys Leu Ala Gln Ser Pro Gln Leu Tyr Lys Gln Met Ala Ile Ser
122 290 295 300

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124 Gly Gly Phe Glu Arg Val Phe Glu Val Gly Pro Val Phe Arg Ala Glu
125 305                               310                               315                               320
127 Asn Ser Asn Thr His Arg His Leu Cys Glu Phe Val Gly Leu Asp Ala
128                               325                               330                               335
130 Glu Met Glu Ile Lys Glu His Tyr Phe Glu Val Cys Asp Ile Ile Asp
131                               340                               345                               350
133 Gly Leu Phe Val Ser Ile Phe Lys His Leu Ser Glu Asn Cys Lys Lys
134                               355                               360                               365
136 Glu Leu Glu Ser Ile Asn Arg Gln Tyr Pro Phe Glu Pro Leu Lys Tyr
137                               370                               375                               380
139 Leu Asp Lys Thr Phe Lys Leu Thr Tyr Glu Glu Gly Ile Gln Met Leu
140 385                               390                               395                               400
142 Lys Glu Ala Gly Thr Glu Ile Glu Pro Met Gly Asp Leu Asn Thr Glu
143                               405                               410                               415
145 Ala Glu Lys Lys Leu Gly Arg Leu Val Arg Glu Lys Tyr Asp Thr Asp
146                               420                               425                               430
148 Phe Phe Ile Leu Tyr Arg Tyr Pro Leu Ala Val Arg Pro Phe Tyr Thr
149                               435                               440                               445
151 Met Pro Cys Tyr Asp Asn Pro Ala Tyr Thr Asn Ser Phe Asp Val Phe
152                               450                               455                               460
154 Ile Arg Gly Glu Glu Ile Ile Ser Gly Ala Gln Arg Ile His Thr Pro
155 465                               470                               475                               480
157 Glu Leu Leu Ala Lys Arg Ala Thr Glu Cys Gly Ile Asp Val Ser Thr
158                               485                               490                               495
160 Ile Ser Ala Tyr Ile Glu Ser Phe Ser Tyr Gly Val Pro Pro His Gly
161                               500                               505                               510
163 Gly Phe Gly Val Gly Leu Glu Arg Val Val Met Leu Phe Cys Ala Leu
164                               515                               520                               525
166 Asn Asn Ile Arg Lys Thr Ser Leu Phe Pro Arg Asp Pro Gln Arg Leu
167                               530                               535                               540
169 Val Pro
170 545
172 <210> SEQ ID NO: 3
173 <211> LENGTH: 730
174 <212> TYPE: DNA
175 <213> ORGANISM: Oryza sativa
177 <400> SEQUENCE: 3
178 gcacgagctt acacggcacg agcttacagg aattcaaagt ctgaaggaag ctggaacaga 60
179 aatcgaaccc atgggtgacc tcaacactga agctgagaaa aaactaggcc ggcttggttaa 120
180 ggagaagtat ggaacagaat ttttcacctt ctatcggtat cctttggctg tgcgtccctt 180
181 ctacaccatg ccttggttatg acaaccacgc ttacagtaac tcttttgatg tctttattcg 240
182 aggagaggaa ataatatctg gagcaciaag aatacattta ccagagctat tgacgaaacg 300
183 tgcaacagag tgtggaattg atgcgagtac tatttcacat tatatcgaat cgttcagcta 360
184 tgggtgcacct cctcatgggtg gttttggtgt cggcctggag aggggtggtaa tgctgttctg 420
185 cgccctaaac aacatcagga agacatcact ttccctcgc gatccacaaa ggctggtgccc 480
186 ataatttgct ttttttccca agagcaaggt ttggactcag tacggactgg gcagttttcc 540
187 tcggctgggt tttttacctg gacattattt tcgtatttat taatgtgctg tactgcaaaa 600
188 cgtgctcctt tccacaacat ttggaatagt tgccgataca tttggaatag ggctcaacgt 660
189 tggcggttgtg atttcgttga tgatcccgcg attcgttaaca aaaaaaaaaa aaaaaaaaaa 720

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190 aaaaaaaaaa                                     730
192 <210> SEQ ID NO: 4
193 <211> LENGTH: 148
194 <212> TYPE: PRT
195 <213> ORGANISM: Oryza sativa
197 <400> SEQUENCE: 4
198 Met Leu Lys Glu Ala Gly Thr Glu Ile Glu Pro Met Gly Asp Leu Asn
199   1           5           10           15
201 Thr Glu Ala Glu Lys Lys Leu Gly Arg Leu Val Lys Glu Lys Tyr Gly
202           20           25           30
204 Thr Glu Phe Phe Ile Leu Tyr Arg Tyr Pro Leu Ala Val Arg Pro Phe
205           35           40           45
207 Tyr Thr Met Pro Cys Tyr Asp Asn Pro Ala Tyr Ser Asn Ser Phe Asp
208           50           55           60
210 Val Phe Ile Arg Gly Glu Ile Ile Ser Gly Ala Gln Arg Ile His
211   65           70           75           80
213 Leu Pro Glu Leu Leu Thr Lys Arg Ala Thr Glu Cys Gly Ile Asp Ala
214           85           90           95
216 Ser Thr Ile Ser Ser Tyr Ile Glu Ser Phe Ser Tyr Gly Ala Pro Pro
217           100          105          110
219 His Gly Gly Phe Gly Val Gly Leu Glu Arg Val Val Met Leu Phe Cys
220           115          120          125
222 Ala Leu Asn Asn Ile Arg Lys Thr Ser Leu Phe Pro Arg Asp Pro Gln
223           130          135          140
225 Arg Leu Val Pro
226 145
228 <210> SEQ ID NO: 5
229 <211> LENGTH: 1109
230 <212> TYPE: DNA
231 <213> ORGANISM: Glycine max
233 <400> SEQUENCE: 5
234 gcacgagggtc atcagagaga atggcttcac cgttcaatgc ttggtgcagg cgcaggccga 60
235 tacggtgagc cgcagatgg tgaagtctgc cgctgcactc agccgcgagt ccatcgctga 120
236 tgtcgaaggc gttgtttcga tccccctcgc tcccatcaaa ggcgccacac aacaggtgga 180
237 aattcaagtg aggaagtgtg attgtgtcag tagggctgta cctactctgc ctattaatct 240
238 tgaggatgct gctcgaagtg aagttgaaat cgagacggct cttcaggctg gtgagcaact 300
239 tgttcgtgtt aatcaggata cacgtctgaa ctttaggggtg cttgatgtgc gaacgccagc 360
240 taatcaaggg attttccgca ttcagtctca agttggaaat gcgttttagac aattcttatt 420
241 atctgaaggt ttttgtgaaa tccacactcc aaagttgata gctggatcta gtgagggagg 480
242 agctgctgtt tttagactgg actacaaagg tcaacctgca tgcctggccc agtcacctca 540
243 gcttcacaag caaatgtcta tttgtggaga ttttggccgt gtttttgaga ttggtcctgt 600
244 gtttagagca gaagattcct acactcacag gcactctgtg gagtttacag gtcttgatgt 660
245 tgaaatggag attaagaagc attactttga ggttatggat atagtcgata gattgtttgt 720
246 cgcaatgttt gacagtttga accagaattg taagaaggat ctggaagctg tcgggtctca 780
247 gtatccattt gaacctttga agtatctgcg gacgacacta cggcttacat atgaagaagg 840
248 gattcagatg ctcaaggatg ttggagtaga aattgaacct tatggtgact tgaataactga 900
249 agcggaaaagg aaattgggtc agctagcttc agagaaatat ggcacagagt tctatatcct 960
250 tcaccgggtac cctttggctg taaggccatt ctatacaatg ccttgctacg acaatcctgc 1020
251 atacagcaac tcgtttgatg tctttattcg aggtgaggag ataatttcag gagctcagcg 1080

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Output Set: N:\CRF3\03112002\I846589A.raw

1109

```

252 tgttcatgtg ccagaatttt tggaacaag
254 <210> SEQ ID NO: 6
255 <211> LENGTH: 369
256 <212> TYPE: PRT
257 <213> ORGANISM: Glycine max
259 <400> SEQUENCE: 6
260 His Glu Val Ile Arg Glu Asn Gly Phe Thr Val Gln Cys Leu Val Gln
261   1           5           10           15
263 Ala Gln Ala Asp Thr Val Ser Pro Gln Met Val Lys Phe Ala Ala Ala
264           20           25           30
266 Leu Ser Arg Glu Ser Ile Val Asp Val Glu Gly Val Val Ser Ile Pro
267           35           40           45
269 Ser Ala Pro Ile Lys Gly Ala Thr Gln Gln Val Glu Ile Gln Val Arg
270           50           55           60
272 Lys Leu Tyr Cys Val Ser Arg Ala Val Pro Thr Leu Pro Ile Asn Leu
273           65           70           75           80
275 Glu Asp Ala Ala Arg Ser Glu Val Glu Ile Glu Thr Ala Leu Gln Ala
276           85           90           95
278 Gly Glu Gln Leu Val Arg Val Asn Gln Asp Thr Arg Leu Asn Phe Arg
279           100          105          110
281 Val Leu Asp Val Arg Thr Pro Ala Asn Gln Gly Ile Phe Arg Ile Gln
282           115          120          125
284 Ser Gln Val Gly Asn Ala Phe Arg Gln Phe Leu Leu Ser Glu Gly Phe
285           130          135          140
287 Cys Glu Ile His Thr Pro Lys Leu Ile Ala Gly Ser Ser Glu Gly Gly
288          145          150          155          160
290 Ala Ala Val Phe Arg Leu Asp Tyr Lys Gly Gln Pro Ala Cys Leu Ala
291           165          170          175
293 Gln Ser Pro Gln Leu His Lys Gln Met Ser Ile Cys Gly Asp Phe Gly
294           180          185          190
296 Arg Val Phe Glu Ile Gly Pro Val Phe Arg Ala Glu Asp Ser Tyr Thr
297           195          200          205
299 His Arg His Leu Cys Glu Phe Thr Gly Leu Asp Val Glu Met Glu Ile
300          210          215          220
302 Lys Lys His Tyr Phe Glu Val Met Asp Ile Val Asp Arg Leu Phe Val
303          225          230          235          240
305 Ala Met Phe Asp Ser Leu Asn Gln Asn Cys Lys Lys Asp Leu Glu Ala
306           245          250          255
308 Val Gly Ser Gln Tyr Pro Phe Glu Pro Leu Lys Tyr Leu Arg Thr Thr
309           260          265          270
311 Leu Arg Leu Thr Tyr Glu Glu Gly Ile Gln Met Leu Lys Asp Val Gly
312           275          280          285
314 Val Glu Ile Glu Pro Tyr Gly Asp Leu Asn Thr Glu Ala Glu Arg Lys
315          290          295          300
317 Leu Gly Gln Leu Val Ser Glu Lys Tyr Gly Thr Glu Phe Tyr Ile Leu
318          305          310          315          320
320 His Arg Tyr Pro Leu Ala Val Arg Pro Phe Tyr Thr Met Pro Cys Tyr
321           325          330          335
323 Asp Asn Pro Ala Tyr Ser Asn Ser Phe Asp Val Phe Ile Arg Gly Glu

```

VERIFICATION SUMMARY

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DATE: 03/11/2002

TIME: 09:44:17

Input Set : A:\BB-1191 Seq List.txt

Output Set: N:\CRF3\03112002\I846589A.raw

L:11 M:270 C: Current Application Number differs, Replaced Application Number  
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:15 M:256 W: Invalid Numeric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD